

Minimal Amounts of Protein Required for Protein Identification Services ***

Information needed	Amount of protein***	Dry / Gel / Membrane / Solution	Digest	Type of service performed
Database Identification of a protein using peptide mass fingerprinting (PMF)	0.5 – 5 pmol	Gel / PVDF Membrane / Solution	Yes	Digest + ZipTip + MALDI-TOF-MS + database search
Database identification of a protein using MS/MS Partial Sequence Data (Sequence Tag)	0.5 – 5 pmol	Gel / Solution	Yes	Digest + o-MALDI (MS/MS + database search) / TOF-TOF or LC-MS/MS (Q-STAR)
N-terminal sequence of a protein	0.5 + pmol	PVDF Membrane / Solution	NO	Edman sequencing using Procise cLC
Internal sequence of a protein (also N-terminally blocked protein)	10 pmol +	Gel / PVDF Membrane/ Solution	Yes	Capillary RP-HPLC followed by Edman sequencing using Procise cLC
C-terminal sequence	~500 pmol	Gel/ Solution	Yes/No	*please inquire regarding instructions for sample preparation
Phosphorylation-site identification	*please inquire	Gel/ Solution	Yes	nano - ESI - precursor ion scanning MS * please inquire
Identification and Quantitative analysis of Differentially expressed proteins using Isotope-Coded Affinity tag chemistry and cleavable-linker technology (ICAT)	100µg Test/Ctrl 300 µg - 500 µg for complex samples (Test/Ctrl)	Dry	Yes	LC-MS/MS (Q-STAR)

*** The amounts of protein are rough estimates of the minimum required for each service. Higher amounts of protein will result in better quality of data and higher probability of a successful identification. MS/MS stands for tandem mass spectrometry.